Attorney Docket No. 5051.458 PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: Hanley-Bowdoin et al.
Application Serial No. 09/289,346
Filed: April 9, 1999

October 3, 2003

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Declaration of Linda Hanley-Bowdoin, Ph.D.

under 37 C.F.R § 1.132

I, Linda Hanley-Bowdoin, Ph.D., do hereby declare and say as follows:

1. I am a named inventor on U.S. Patent Application Serial No. 09/289,346 (*hereinafter* "the '346 application").

2. The '646 application describes the identification and characterization of several mutants of the geminivirus AL1/C1 protein for the ability to increase resistance in plants to infection by a geminivirus.

3. The nucleotide sequences of the mutants described in this invention are set forth in Table 4. The nucleotide sequences encode the amino acid sequences of the respective mutants described in the specification.

4. For mutants Ala2 and Leu, the nucleotide sequences that respectively encode the amino acid sequence of Ala2, as set forth in the Sequence Listing as SEQ ID NO:12 and Leu, as set forth in the Sequence Listing as SEQ ID NO:10 were identified prior to the filing of this application to be CAGCGTCGTTgctaGcTgcGCAACCTCCTCTAGCA (Ala2) and GAAGCATTTAAgGCCTCTagTagAagGTCGTTAGATG (Leu). These sequences are shown in the data sheets attached as Exhibits A and B, which were derived from the original sequencing data obtained prior to the filing date of this application. In particular, the relevant nucleotide sequences as

highlighted and the complementary nucleotide sequence is written in pencil above the printed sequence. This written sequence is the correct version of the coding sequence shown in Table 4 of the specification.

5. The respective nucleotide sequences for mutants Ala2 and Leu as shown in Table 4 in the specification as originally filed have the following errors. The amendments to these sequences are shown herein in standard amendment format (i.e., underline to add and double bracket to delete):

CAGCGTCGTTgctaGcTgcGCAACCTCCTCTAGCA (Ala2)

GAAGCA[[A]]TTTAAgGCCTCTagTagAagGTCGTTAGATG (Leu)

6. As the correct nucleotide sequences for mutants Ala2 and Leu were known prior to the filing of this application, the errors in these sequences as set forth in Table 4 are inadvertent typographical errors. These errors were readily detected when an attempt was made to translate the sequences as originally set forth in Table 4 into amino acid sequences. The particular errors were readily identified and once the sequences were corrected as described above, the nucleotide sequences of mutants Ala2 and Leu were translated properly into the correct amino acid sequences identified for these mutants and as disclosed in the specification as filed.

7. I do hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 19 of the United States Code an that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Linda Hanley-Bowdoin

Linda Hanley-Bowdoin, Ph.D.

10-3-03

Date

Attachments: Exhibits A and B

Ala2

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1546 ATGCCATCGCATCCAAAACGGTTTCAAATAAATGCCAAAAATTATTTTCTTACATATCCTCAGTGCTCCTTGTCCAAAGA
   1 MetProSerHisProLysArgPheGlnIleAsnAlaLysAsnTyrPheLeuThrTyrProGlnCysSerLeuSerLysGl

1626 AGAATCACTTTCTCAATTACAAGCCCTAAACACTCCGATTAACAAAAAATTCATAAAAATCTGCAGAGAGCTTCATGAAG
  27 uGluSerLeuSerGlnLeuGlnAlaLeuAsnThrProIleAsnLysLysPheIleLysIleCysArgGluLeuHisGluA

1706 ATGGGCAACCTCACCTCCACGTGCTTATTCAGTTCGAGGGAAAATACTGCTGCCAAAATCAACGATTCTTCGACCTGGTAT
  54 spGlyGlnProHisLeuHisValLeuIleGlnPheGluGlyLysTyrCysCysGlnAsnGlnArgPhePheAspLeuVal S

1787 CCCCAACAAGGTCAGCACATTTCCATCCAAACATTCAGAGAGCTAAATCGTCTTCCGACGTCAAGACGTACATCGACAAAG
  81 erProThrArgSerAlaHisPheHisProAsnIleGlnArgAlaLysSerSerSerAspValLysThrTyrIleAspLysA

                                    SalI                                    NheI
1868 ACGGAGATACTCTTGTATGGGGAGAATTCCAGGTCGACGGTCGAAGTGCTAGAGGAGGTTGCGCAGCTAGCAACGACGCTG
 108 spGlyAspThrLeuValTrpGlyGluPheGlnValAspGlyArgSerAlaArgGlyGlyCysAlaAlaSerAsnAspAlaA

1949 CAGCAGAGGCGTTAAATGCTTCTTCCAAAGAAGAAGCCCTGCAGATAATTAGAGAGAAAATCCCAGAAAAATATTTATTTC
 135 laAlaGluAlaLeuAsnAlaSerSerLysGluGluAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPheG

                                                    NcoI
2030 AGTTCCACAATCTAAATAGCAATTTAGATAGGATATTTGATAAGACTCCTGAACCATGGCTTCCTCCGTTCCACGTCTCAT
 162 lnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrProGluProTrpLeuProProPheHisValSer S

2111 CATTTACTAACGTGCCAGACGAGATGAGACAATGGGCTGAAAATTATTTTGGAAAGAGTTCCGCTGCGCGGCCGGAGAGAC
 189 erPheThrAsnValProAspGluMetArgGlnTrpAlaGluAsnTyrPheGlyLysSerSerAlaAlaArgProGluArgP

2192 CTATTAGTATTATCATCGAGGGCGATAGTCGGACGGGAAAGACTATGTGGGCTCGTTCACTAGGCCCACATAATTATTTG
 216 rolleSerIleIleIleIleGluGlyAspSerArgThrGlyLysThrMetTrpAlaArgSerLeuGlyProHisAsnTyrLeu

2272 AGCGGGCATTTGGATCTCAATTCTAGGGTTTACTCAAACAAGGTTGAGTATAACGTCATCGATGATGTCACACCGCAATAT
 243 SerGlyHisLeuAspLeuAsnSerArgValTyrSerAsnLysValGluTyrAsnValIleAspAspValThrProGlnTyr

2353 CTAAAGTTGAAACATTGGAAAGAACTCATTGGGGCCCAAAGAGATTGGCAGACTAACTGTAAATACGGAAAGCCAGTTCAA
 270 LeuLysLeuLysHisTrpLysGluLeuIleGlyAlaGlnArgAspTrpGlnThrAsnCysLysTyrGlyLysProValGln

                                                    NheI
2434 ATTAAAGGAGGTATCCCGTCAATCGTGCTGTGCAATCCTGGAGAGGGTGCTAGCTATAAAGTTTTCCTCGACAAAGAGGAA
 297 IleLysGlyGlyIleProSerIleValLeuCysAsnProGlyGluGlyAlaSerTyrLysValPheLeuAspLysGluGlu

2515 AACACTCCACTAAAGAACTGGACTTTCCATAATGCGAAATTCGTCTTCCTCAACTCCCCCCTCTATCAAAGCTCAACACA
 324 AsnThrProLeuLysAsnTrpThrPheHisAsnAlaLysPheValPheLeuAsnSerProLeuTyrGlnSerSerThrGl

2595 GAGCAGC
 350 nSerSer
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Leu2-

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1095 ATGCCATCGCATCCAAAACGGTTTCAAATAAATGCCAAAAATTATTTTCTTACATATCCTCAGTGCTCCTTGT
   1▶MetProSerHisProLysArgPheGlnIleAsnAlaLysAsnTyrPheLeuThrTyrProGlnCysSerLeuS

1168 CCAAAGAAGAATCACTTTCTCAATTACAAGCCCTAAACACTCCGATTAACAAAAAATTCATAAAAATCTGCAG
  25▶erLysGluGluSerLeuSerGlnLeuGlnAlaLeuAsnThrProIleAsnLysLysPheIleLysIleCysAr

1241 AGAGCTTCATGAAGATGGGCAACCTCACCTCCACGTGCTTATTCAGTTCGAGGGAAAATACTGCTGCCAAAAT
  49▶gGluLeuHisGluAspGlyGlnProHisLeuHisValLeuIleGlnPheGluGlyLysTyrCysCysGlnAsn

1314 CAACGATTCTTCGACCTGGTATCCCCAACAAGGTCAGCACATTTCCATCCAAACATTCAGAGAGCTAAATCGT
  74▶GlnArgPhePheAspLeuValSerProThrArgSerAlaHisPheHisProAsnIleGlnArgAlaLysSerS

                                                                    EcoRI
1387 CTTCCGACGTCAAGACGTACATCGACAAAGACGGAGATACTCTTGTATGGGGAGAATTCCAGGTCGACGGTCG
  98▶erSerAspValLysThrTyrIleAspLysAspGlyAspThrLeuValTrpGlyGluPheGlnValAspGlyAr

                                    GTAGATTGCTGGAAGATGATCTCCGGAATTTACGAAG  StuI
1460 AAGTGCTAGAGGAGGTTGCCAAACATCTAACGACCTTCTACTAGAGGCCTTAAATGCTTCTTCCAAAGAAGAA
 122▶gSerAlaArgGlyGlyCysGlnThrSerAsnAspLeuLeuLeuGluAlaLeuAsnAlaSerSerLysGluGlu

1533 GCCCTGCAGATAATTAGAGAGAAAATCCCAGAAAAATATTTATTTCAGTTCCACAATCTAAATAGCAATTTAG
 147▶AlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPheGlnPheHisAsnLeuAsnSerAsnLeuA

1606 ATAGGATATTTGATAAGACTCCTGAACCATGGCTTCCTCCGTTCCACGTCTCATCATTTACTAACGTGCCAGA
 171▶spArgIlePheAspLysThrProGluProTrpLeuProProPheHisValSerSerPheThrAsnValProAs

                                                                    EagI
1679 CGAGATGAGACAATGGGCTGAAAATTATTTTGGAAAGAGTTCCGCTGCGCGGCCGGAGAGACCTATTAGTATT
 195▶pGluMetArgGlnTrpAlaGluAsnTyrPheGlyLysSerSerAlaAlaArgProGluArgProIleSerIle

1752 ATCATCGAGGGCGATAGTCGGACGGGAAAGACTATGTGGGCTCGTTCACTAGGCCCACATAATTATTTGAGCG
 220▶IleIleGluGlyAspSerArgThrGlyLysThrMetTrpAlaArgSerLeuGlyProHisAsnTyrLeuSerG

1825 GGCATTTGGATCTCAATTCTAGGGTTTACTCAAACAAGGTTGAGTATAACGTCATCGATGATGTCACACCGCA
 244▶lyHisLeuAspLeuAsnSerArgValTyrSerAsnLysValGluTyrAsnValIleAspAspValThrProGl

1898 ATATCTAAAGTTGAAACATTGGAAAGAACTCATTGGGGCCCAAAGAGATTGGCAGACTAACTGTAAATACGGA
 268▶nTyrLeuLysLeuLysHisTrpLysGluLeuIleGlyAlaGlnArgAspTrpGlnThrAsnCysLysTyrGly

1971 AAGCCAGTTCAAATTAAAGGAGGTATCCCGTCAATCGTGCTGTGCAATCCTGGAGAGGGTGCTAGCTATAAAG
 293▶LysProValGlnIleLysGlyGlyIleProSerIleValLeuCysAsnProGlyGluGlyAlaSerTyrLysV

2044 TTTTCCTCGACAAAGAGGAAAACACTCCACTAAAGAACTGGACTTTCCATAATGCGAAATTCGTCTTCCTCAA
 317▶alPheLeuAspLysGluGluAsnThrProLeuLysAsnTrpThrPheHisAsnAlaLysPheValPheLeuAs

2117 CTCCCCCCTCTATCAAAGCTCAACACAGAGCAGC
 341▶nSerProLeuTyrGlnSerSerThrGlnSerSer
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